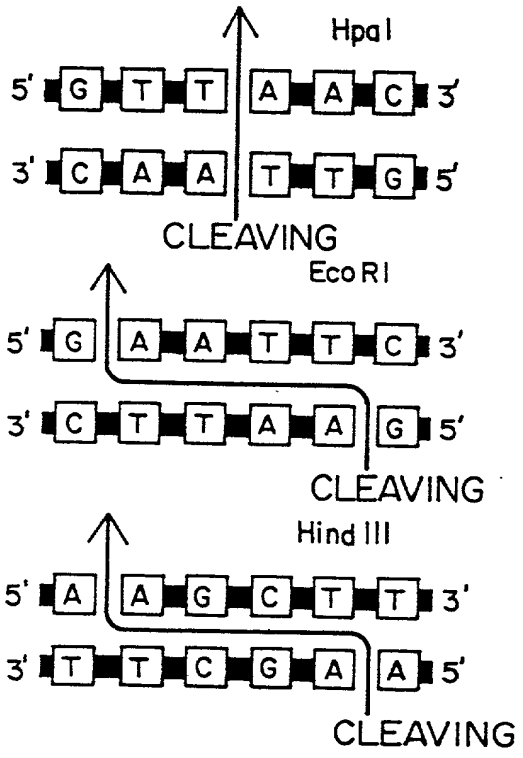
Hpa I
5' G T T A A C 3'
3' C A A T T G 5'
CLEAVING
EcoRI
5' G A A T T C 3'
3' C T T A A G 5'
CLEAVING
Hind III
5' A A G C T T 3'
3' T T C G A A 5'
CLEAVING

FIG. 1

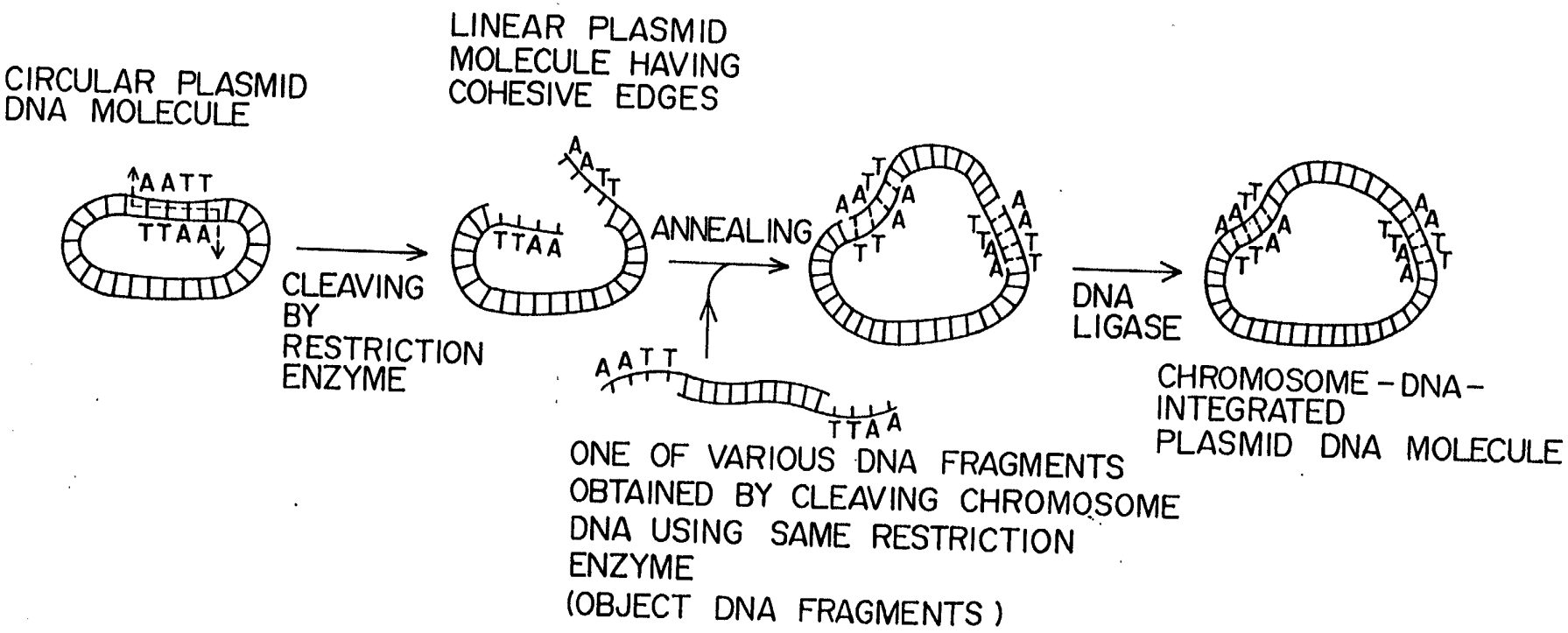

FIG. 2

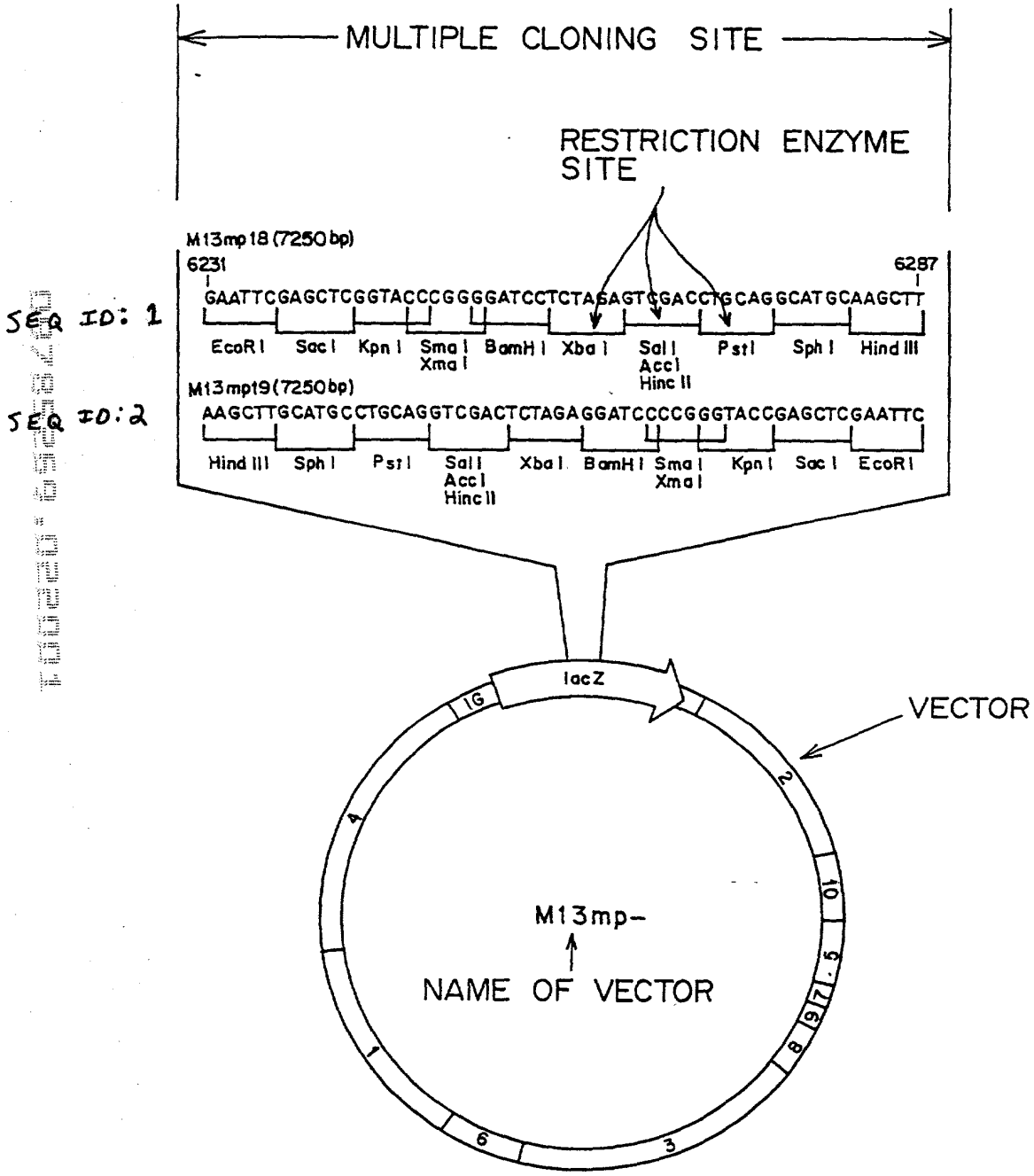
MULTIPLE CLONING SITE
RESTRICTION ENZYME SITE
M13mp18 (7250 bp)
6231
6287
GAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTT
EcoR I
Sac I
Kpn I
Sma I
Xma I
BamH I
Xba I
Sal I
Acc I
Hinc II
Pst I
Sph I
Hind III
M13mp19 (7250 bp)
AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTC
Hind III
Sph I
Pst I
Sal I
Acc I
Hinc II
Xba I
BamH I
Sma I
Xma I
Kpn I
Sac I
EcoR I
SEQ ID: 1
SEQ ID: 2
lacZ
IG
VECTOR
M13mp-
NAME OF VECTOR
1
2
3
4
5
6
7
8
9
10

FIG. 3

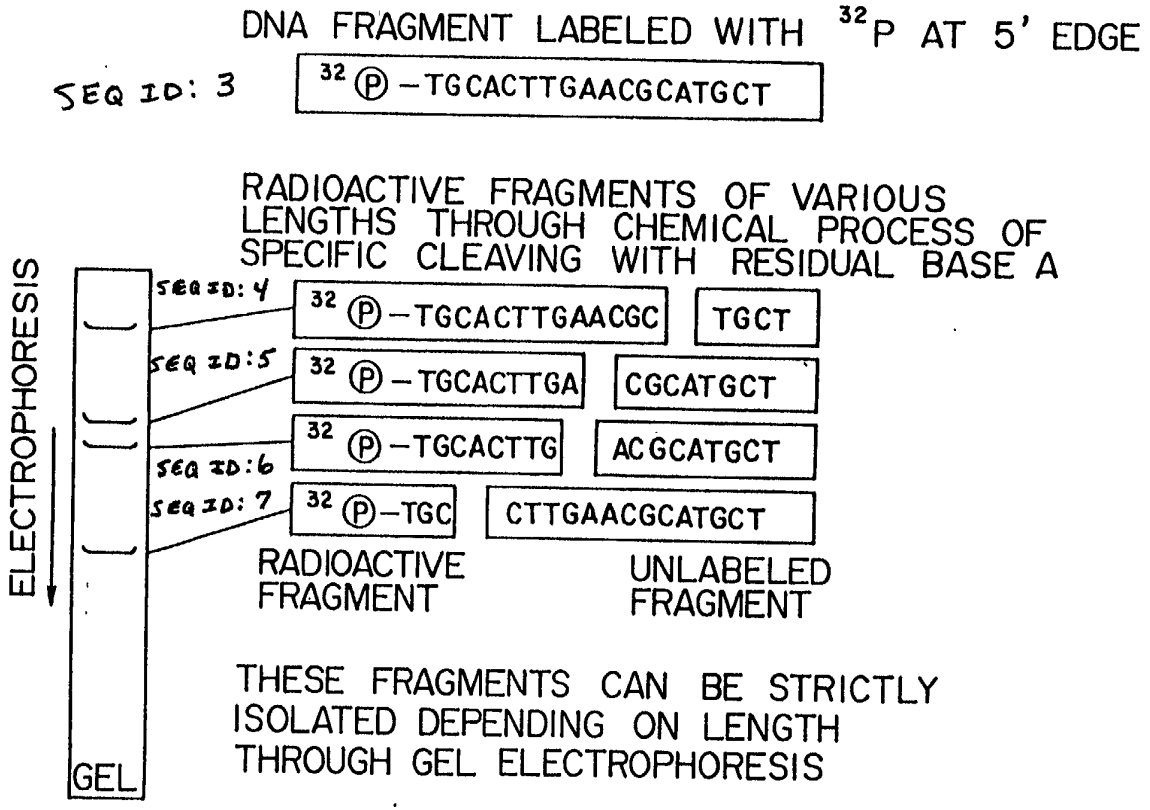

FIG. 4

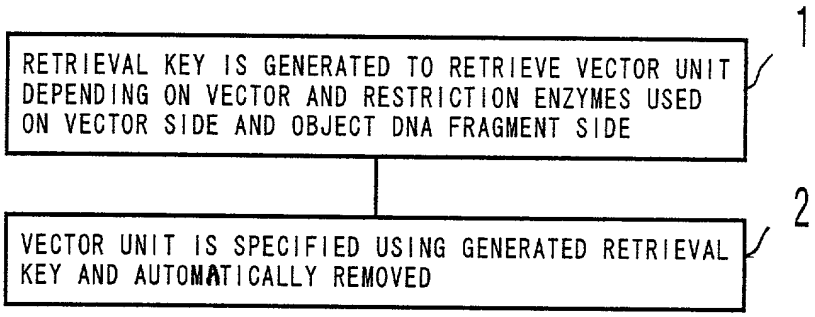
RETRIEVAL KEY IS GENERATED TO RETRIEVE VECTOR UNIT DEPENDING ON VECTOR AND RESTRICTION ENZYMES USED ON VECTOR SIDE AND OBJECT DNA FRAGMENT SIDE
1
VECTOR UNIT IS SPECIFIED USING GENERATED RETRIEVAL KEY AND AUTOMATICALLY REMOVED
2

FIG. 5

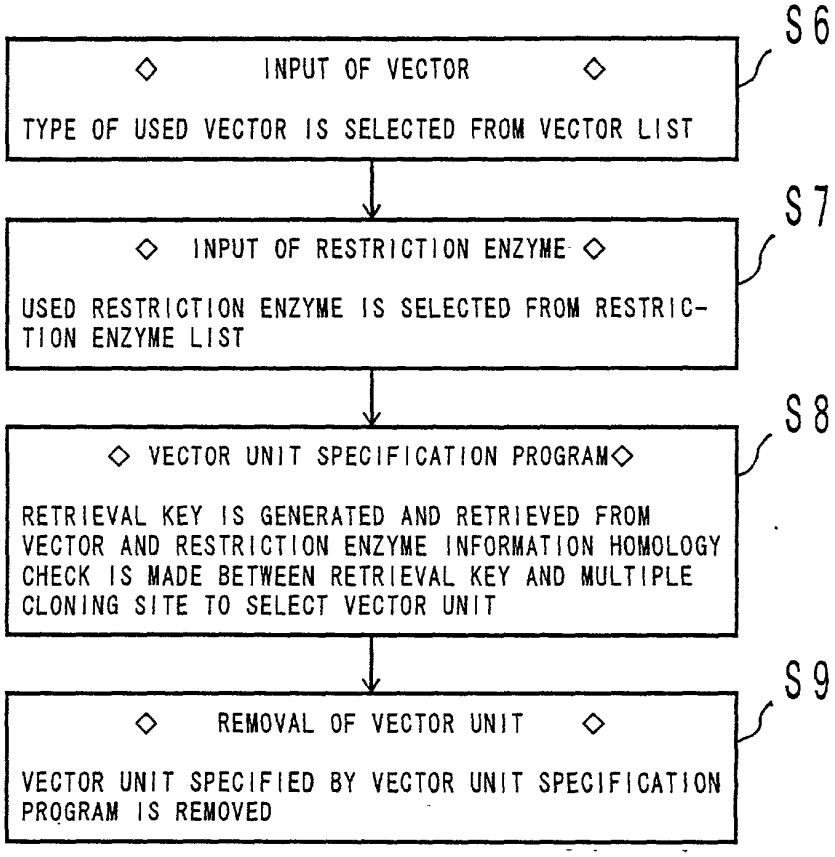
S6
◇ INPUT OF VECTOR ◇
TYPE OF USED VECTOR IS SELECTED FROM VECTOR LIST
S7
◇ INPUT OF RESTRICTION ENZYME ◇
USED RESTRICTION ENZYME IS SELECTED FROM RESTRICTION ENZYME LIST
S8
◇ VECTOR UNIT SPECIFICATION PROGRAM◇
RETRIEVAL KEY IS GENERATED AND RETRIEVED FROM VECTOR AND RESTRICTION ENZYME INFORMATION HOMOLOGY CHECK IS MADE BETWEEN RETRIEVAL KEY AND MULTIPLE CLONING SITE TO SELECT VECTOR UNIT
S9
◇ REMOVAL OF VECTOR UNIT ◇
VECTOR UNIT SPECIFIED BY VECTOR UNIT SPECIFICATION PROGRAM IS REMOVED

FIG. 6

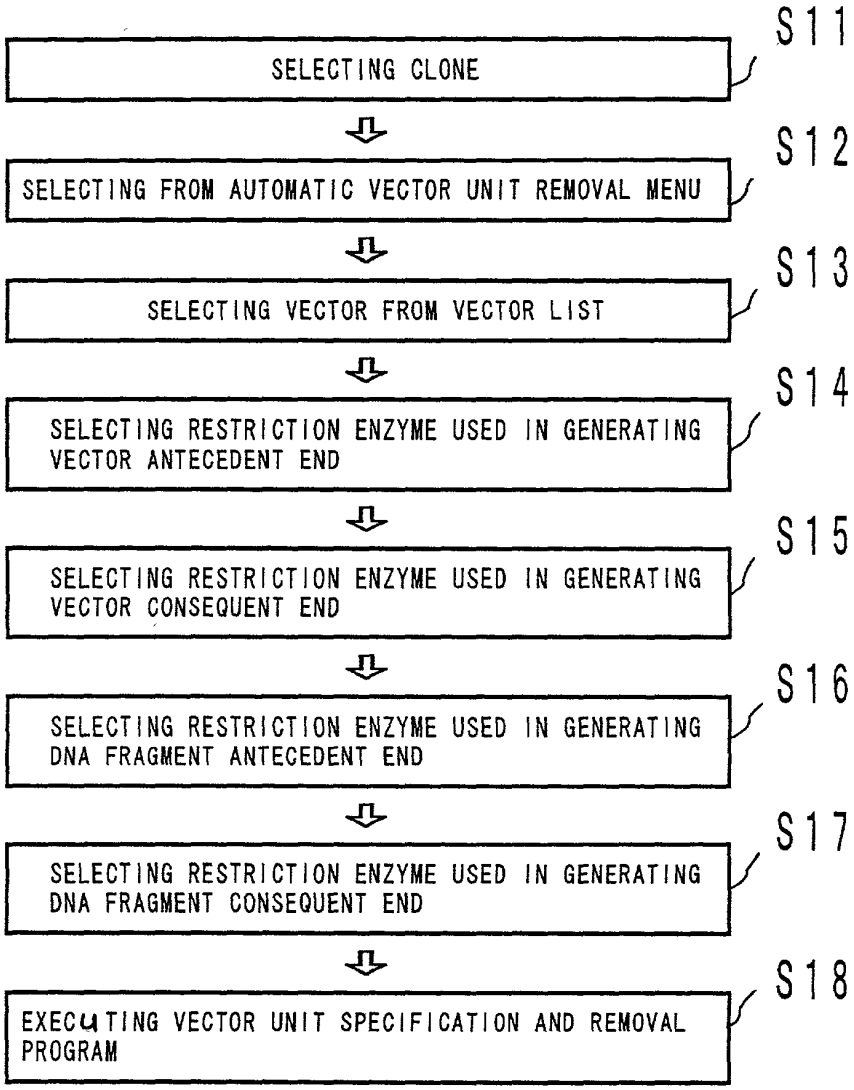
S11
SELECTING CLONE
S12
SELECTING FROM AUTOMATIC VECTOR UNIT REMOVAL MENU
S13
SELECTING VECTOR FROM VECTOR LIST
S14
SELECTING RESTRICTION ENZYME USED IN GENERATING VECTOR ANTECEDENT END
S15
SELECTING RESTRICTION ENZYME USED IN GENERATING VECTOR CONSEQUENT END
S16
SELECTING RESTRICTION ENZYME USED IN GENERATING DNA FRAGMENT ANTECEDENT END
S17
SELECTING RESTRICTION ENZYME USED IN GENERATING DNA FRAGMENT CONSEQUENT END
S18
EXECUTING VECTOR UNIT SPECIFICATION AND REMOVAL PROGRAM

FIG. 7

M13MP18
M13MP19
PBR322
PSL1180
PSL1190
PT7T318U
PT7T319U
PTZ18R
PTZ19R
PUC18
PUC19, ETC.

FIG. 8

VECTOR DB FORMAT

>ID
PUC18
>SEQ ID: 8
TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGA
GCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC
ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGG
GGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGCCAA
GCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAATCATGGTCATAGCTGTTTCCT
GTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATG
AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAAT
GAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG
GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG
AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCC
GCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG
TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC
GGGAAGCGTGGCGCTTTCTCAAAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG
TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC
TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG
GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAG
TTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA
AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGAT
TTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTA
TATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCA
TCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGAT
ACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTC
CTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTG
CGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCA
ACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAA
GTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGC
TTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTC
AATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCT
CAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTC
ACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAAT
ACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA
TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATC
ATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
>MULTI
399..450

FIG. 9

(* INDICATES MULTIPLE CLONING SITE)

****

SEQ ID: 9 GTGCCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAAT

SEQ ID: 10 AAGCTT⇨HIND III

SEQ ID: 11 GCATGC⇨SPH I

SEQ ID: 12 CTGCAG⇨PST I

SEQ ID: 13 GTCGAC⇨SAL I, ACC I, HINC II

SEQ ID: 14 TCTAGA⇨XBA I

SEQ ID: 15 GGATCC⇨BAMH I

SEQ ID: 16 CCCGGG ⇨SMA I, XMA I

SEQ ID: 17 GGTACC ⇨KPN I

SEQ ID: 18 GAGCTC ⇨SAC I

SEQ ID: 19 GAATTC ⇨ECOR I

FIG. 10

VECTOR SIDE	OBJECT DNA FRAGMENT SIDE
HIND III	HINDIII
SPH I	SPH I
PST I	PST I
SAL I	SAL I
ACC I	ACC I
HINC II	HINC II
XBA I	XBA I
BAMH I	BAMH I
SMA I	SMA I
XMA I	XMA I
KPN I	KPN I
SAC I	SAC I
ECOR I	ECOR I
	OTHER RESTRICTION ENZYME
	• • •

FIG. 11

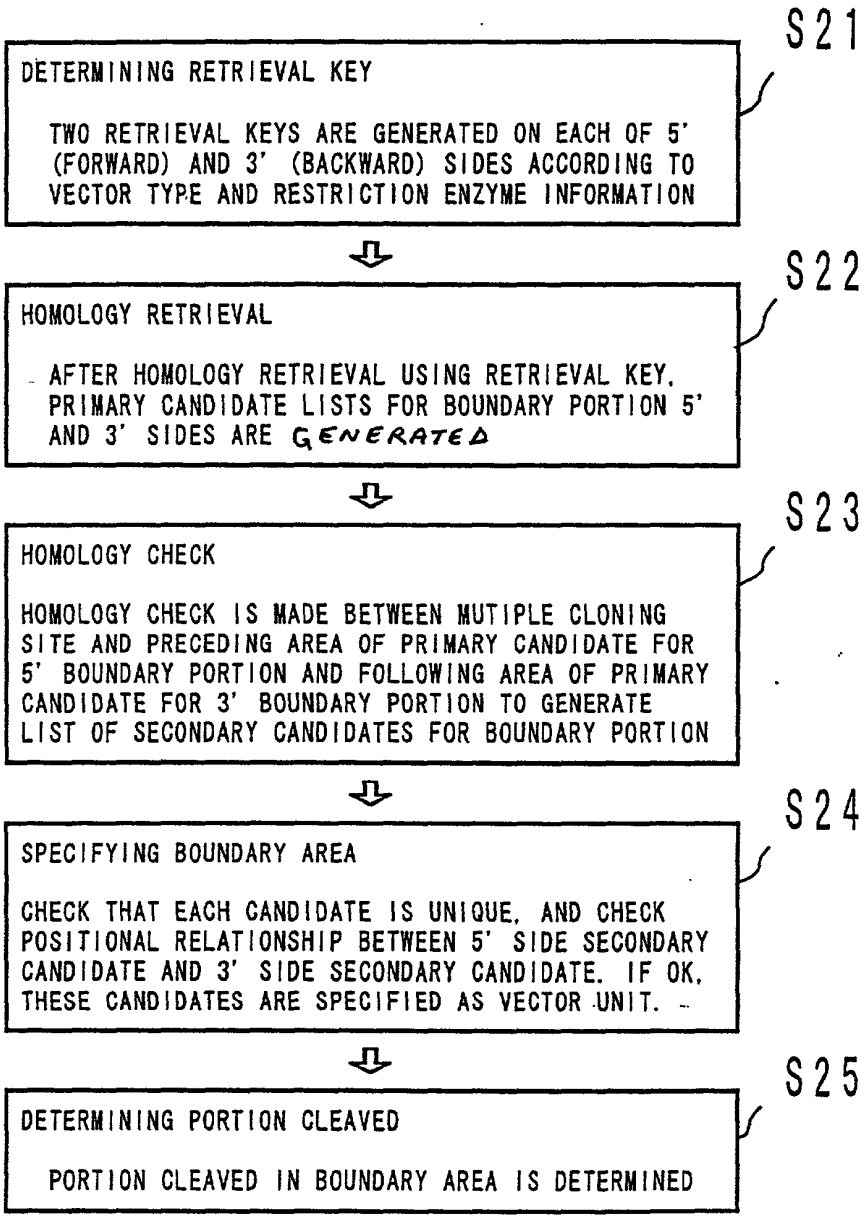
S21
DETERMINING RETRIEVAL KEY
TWO RETRIEVAL KEYS ARE GENERATED ON EACH OF 5' (FORWARD) AND 3' (BACKWARD) SIDES ACCORDING TO VECTOR TYPE AND RESTRICTION ENZYME INFORMATION
S22
HOMOLOGY RETRIEVAL
AFTER HOMOLOGY RETRIEVAL USING RETRIEVAL KEY, PRIMARY CANDIDATE LISTS FOR BOUNDARY PORTION 5' AND 3' SIDES ARE GENERATED
S23
HOMOLOGY CHECK
HOMOLOGY CHECK IS MADE BETWEEN MUTIPLE CLONING SITE AND PRECEDING AREA OF PRIMARY CANDIDATE FOR 5' BOUNDARY PORTION AND FOLLOWING AREA OF PRIMARY CANDIDATE FOR 3' BOUNDARY PORTION TO GENERATE LIST OF SECONDARY CANDIDATES FOR BOUNDARY PORTION
S24
SPECIFYING BOUNDARY AREA
CHECK THAT EACH CANDIDATE IS UNIQUE, AND CHECK POSITIONAL RELATIONSHIP BETWEEN 5' SIDE SECONDARY CANDIDATE AND 3' SIDE SECONDARY CANDIDATE. IF OK, THESE CANDIDATES ARE SPECIFIED AS VECTOR UNIT.
S25
DETERMINING PORTION CLEAVED
PORTION CLEAVED IN BOUNDARY AREA IS DETERMINED

FIG. 12

WHEN SINGLE-STRANDED AREA IS FOUND ON 3' SIDE

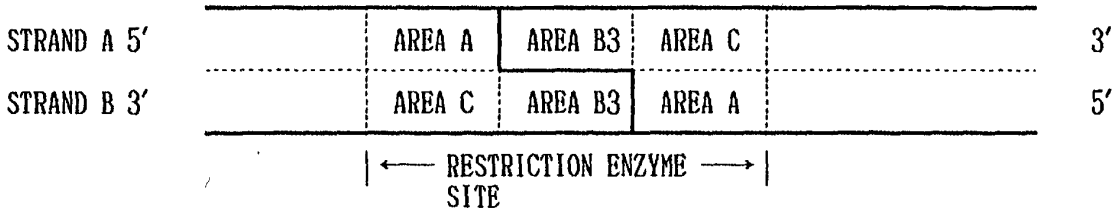

FIG. 13A

WHEN NO SINGLE-STRANDED AREA IS FOUND

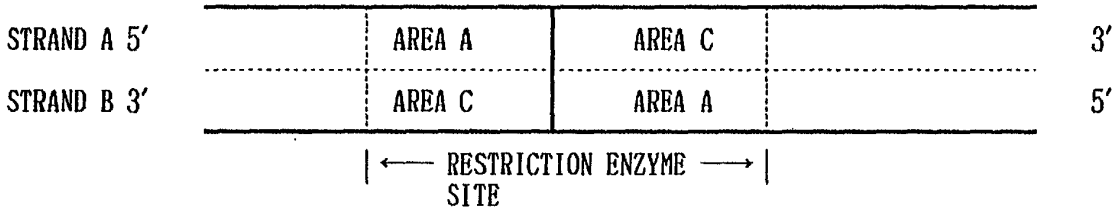

FIG. 13B

WHEN SINGLE-STRANDED AREA IS FOUND ON 5' SIDE

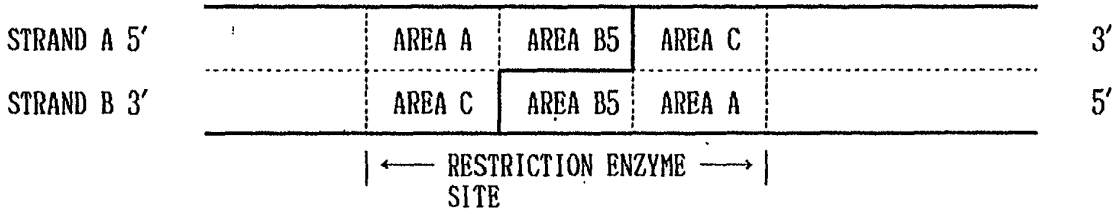

FIG. 13C

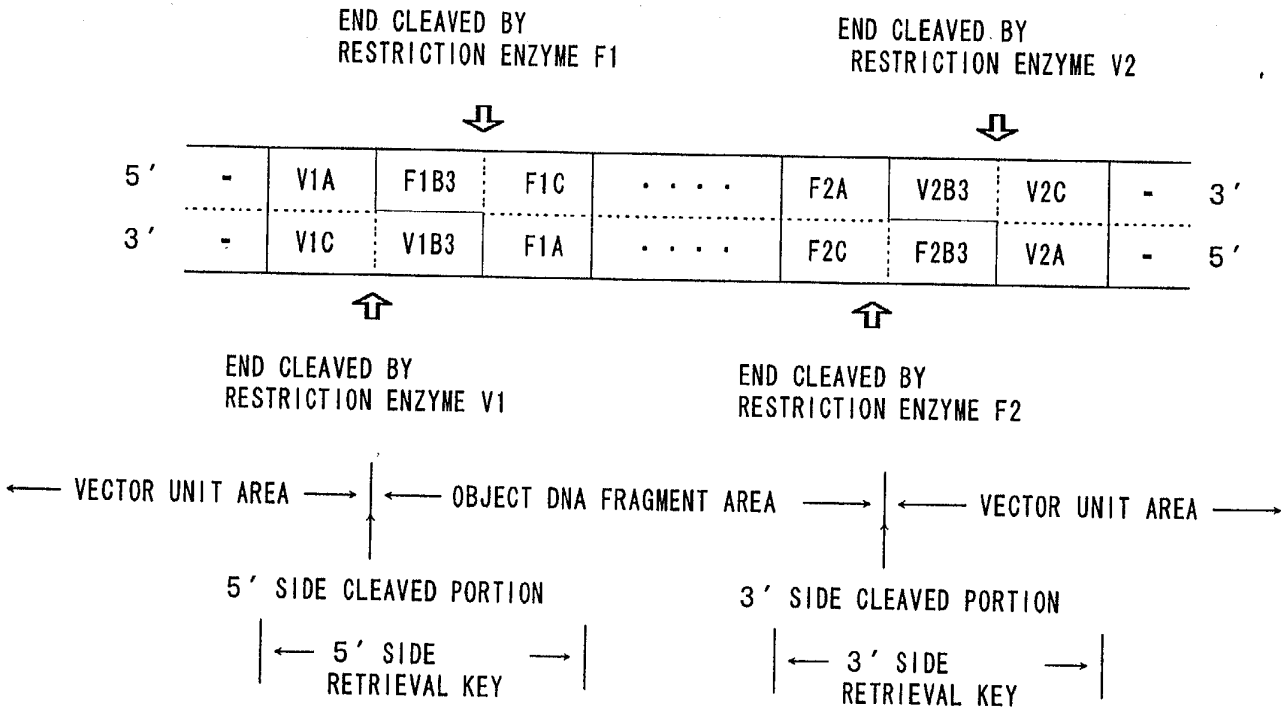
END CLEAVED BY
RESTRICTION ENZYME F1
END CLEAVED BY
RESTRICTION ENZYME V2
5′
3′
-
V1A
F1B3
F1C
F2A
V2B3
V2C
V1C
V1B3
F1A
F2C
F2B3
V2A
END CLEAVED BY
RESTRICTION ENZYME V1
END CLEAVED BY
RESTRICTION ENZYME F2
VECTOR UNIT AREA
OBJECT DNA FRAGMENT AREA
VECTOR UNIT AREA
5′ SIDE CLEAVED PORTION
3′ SIDE CLEAVED PORTION
5′ SIDE
RETRIEVAL KEY
3′ SIDE
RETRIEVAL KEY

FIG. 14

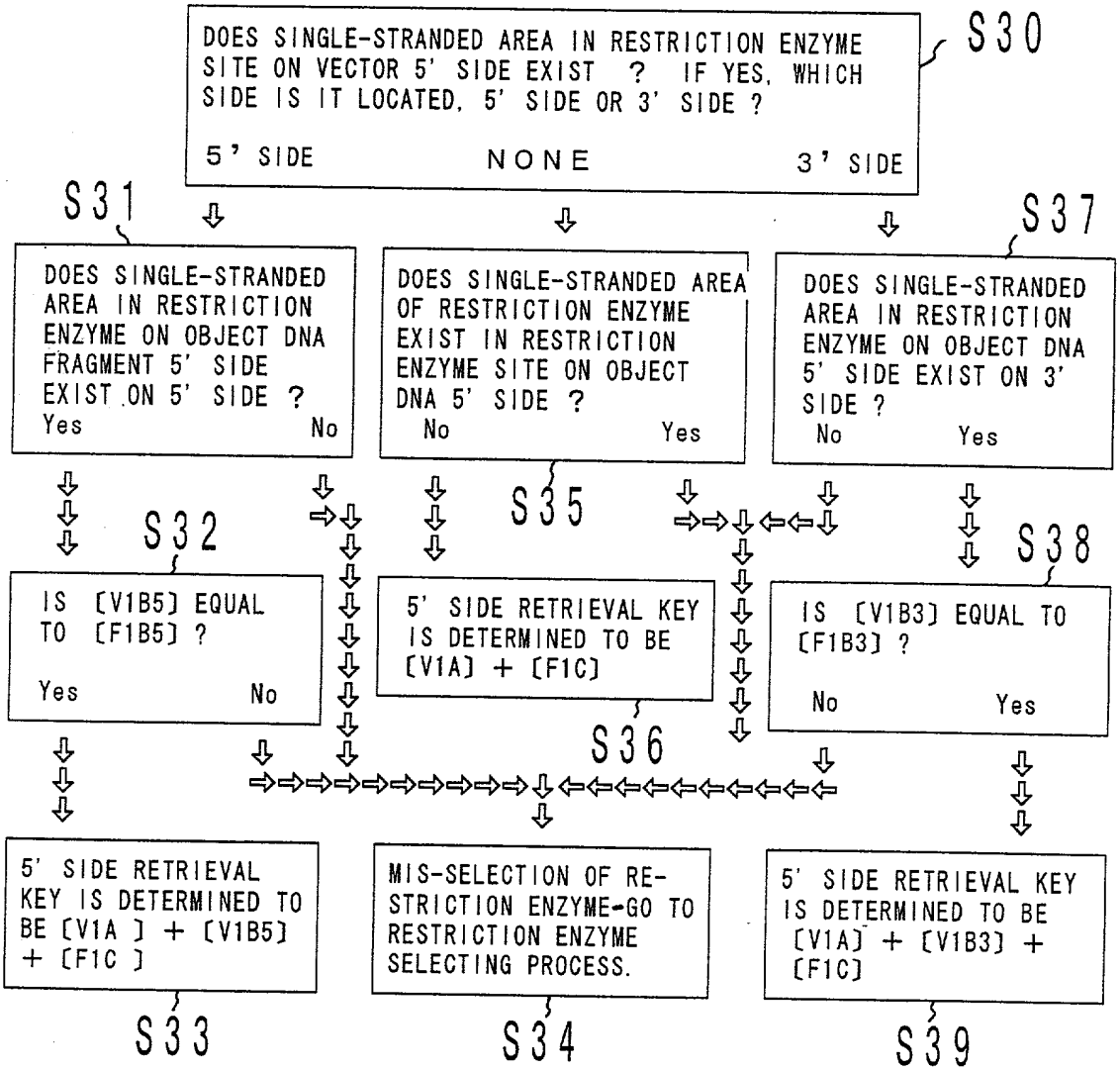
DOES SINGLE-STRANDED AREA IN RESTRICTION ENZYME SITE ON VECTOR 5' SIDE EXIST ? IF YES, WHICH SIDE IS IT LOCATED, 5' SIDE OR 3' SIDE ?
5' SIDE
NONE
3' SIDE
S30
S31
DOES SINGLE-STRANDED AREA IN RESTRICTION ENZYME ON OBJECT DNA FRAGMENT 5' SIDE EXIST ON 5' SIDE ?
Yes
No
S32
IS [V1B5] EQUAL TO [F1B5] ?
Yes
No
5' SIDE RETRIEVAL KEY IS DETERMINED TO BE [V1A] + [V1B5] + [F1C]
S33
DOES SINGLE-STRANDED AREA OF RESTRICTION ENZYME EXIST IN RESTRICTION ENZYME SITE ON OBJECT DNA 5' SIDE ?
No
Yes
S35
5' SIDE RETRIEVAL KEY IS DETERMINED TO BE [V1A] + [F1C]
S36
MIS-SELECTION OF RESTRICTION ENZYME-GO TO RESTRICTION ENZYME SELECTING PROCESS.
S34
S37
DOES SINGLE-STRANDED AREA IN RESTRICTION ENZYME ON OBJECT DNA 5' SIDE EXIST ON 3' SIDE ?
No
Yes
S38
IS [V1B3] EQUAL TO [F1B3] ?
No
Yes
5' SIDE RETRIEVAL KEY IS DETERMINED TO BE [V1A] + [V1B3] + [F1C]
S39

FIG. 15

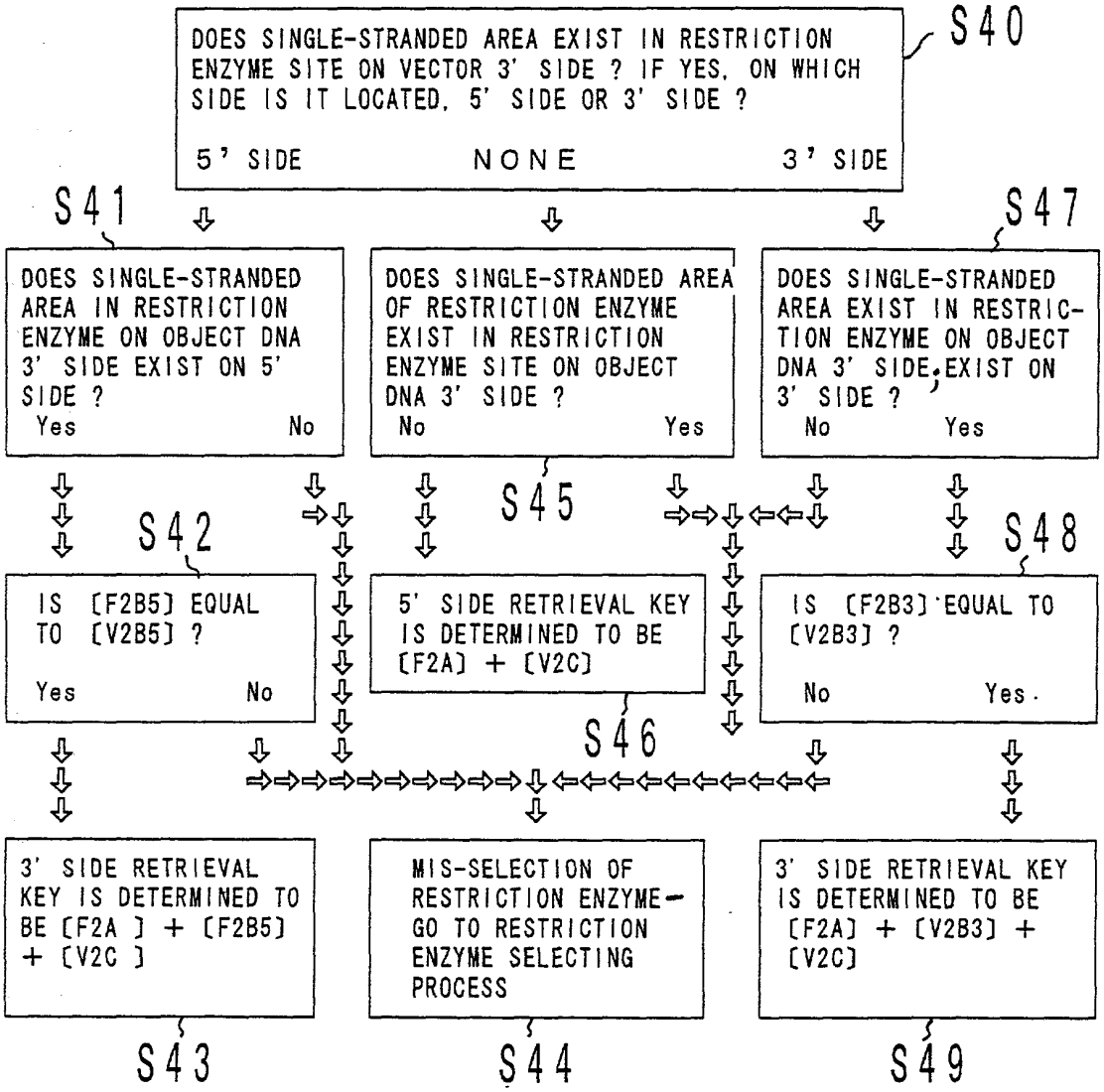
DOES SINGLE-STRANDED AREA EXIST IN RESTRICTION ENZYME SITE ON VECTOR 3' SIDE ? IF YES, ON WHICH SIDE IS IT LOCATED, 5' SIDE OR 3' SIDE ?
5' SIDE
NONE
3' SIDE
S40
S41
S47
DOES SINGLE-STRANDED AREA IN RESTRICTION ENZYME ON OBJECT DNA 3' SIDE EXIST ON 5' SIDE ?
Yes
No
DOES SINGLE-STRANDED AREA OF RESTRICTION ENZYME EXIST IN RESTRICTION ENZYME SITE ON OBJECT DNA 3' SIDE ?
No
Yes
DOES SINGLE-STRANDED AREA EXIST IN RESTRICTION ENZYME ON OBJECT DNA 3' SIDE, EXIST ON 3' SIDE ?
No
Yes
S42
S45
S48
IS [F2B5] EQUAL TO [V2B5] ?
Yes
No
5' SIDE RETRIEVAL KEY IS DETERMINED TO BE [F2A] + [V2C]
IS [F2B3] EQUAL TO [V2B3] ?
No
Yes
S46
3' SIDE RETRIEVAL KEY IS DETERMINED TO BE [F2A] + [F2B5] + [V2C]
MIS-SELECTION OF RESTRICTION ENZYME-GO TO RESTRICTION ENZYME SELECTING PROCESS
3' SIDE RETRIEVAL KEY IS DETERMINED TO BE [F2A] + [V2B3] + [V2C]
S43
S44
S49

FIG. 16

WHEN HIND III IS SPECIFIED ON VECTOR 5' SIDE XBA I IS SPECIFIED ON VECTOR 3' SIDE, HIND III IS SPECIFIED ON OBJECT DNA 5' SIDE, AND XBA I IS SPECIFIED ON OBJECT DNA 3' SIDE

(**** INDICATES RESIDUAL MULTIPLECLONING SITE
(++++ INDICATES AN OBJECT DNA FRAGMENT

```
    *****                          ******************************
GTGCCAAGCTT++++++++++++++++++TCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAAT
    AAGCTT                     TCTAGA
      ⇧                          ⇧
```

5' SIDE RETRIEVAL KEY (IN THIS EXAMPLE, HIND III SITE)

9' SIDE RETRIEVAL KEY (IN THIS EXAMPLE, XBA I SITE)

FIG. 17

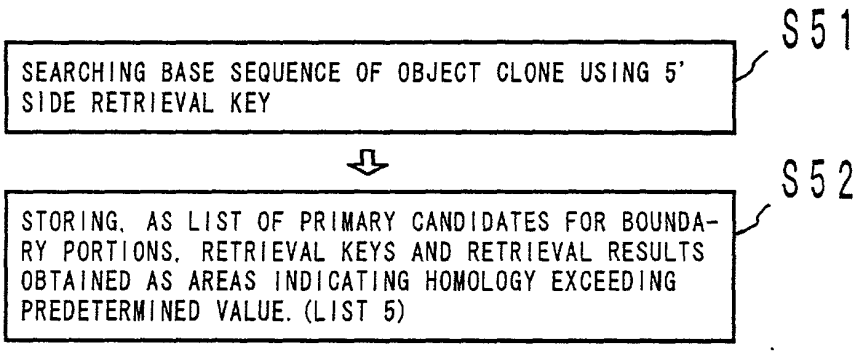
S51
SEARCHING BASE SEQUENCE OF OBJECT CLONE USING 5' SIDE RETRIEVAL KEY
S52
STORING, AS LIST OF PRIMARY CANDIDATES FOR BOUNDARY PORTIONS, RETRIEVAL KEYS AND RETRIEVAL RESULTS OBTAINED AS AREAS INDICATING HOMOLOGY EXCEEDING PREDETERMINED VALUE. (LIST 5)

FIG. 18

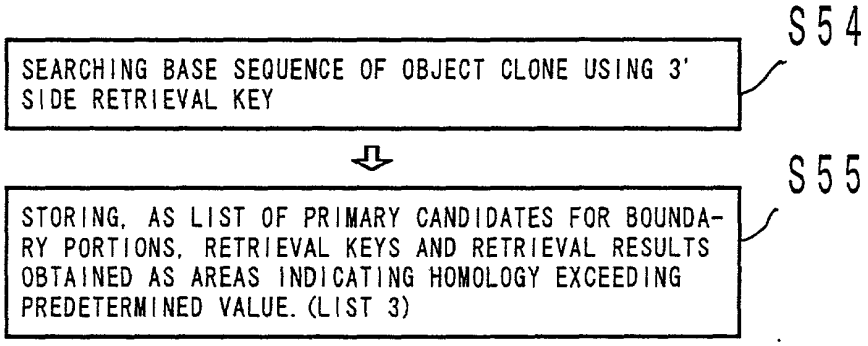
S54
SEARCHING BASE SEQUENCE OF OBJECT CLONE USING 3' SIDE RETRIEVAL KEY
S55
STORING, AS LIST OF PRIMARY CANDIDATES FOR BOUNDARY PORTIONS, RETRIEVAL KEYS AND RETRIEVAL RESULTS OBTAINED AS AREAS INDICATING HOMOLOGY EXCEEDING PREDETERMINED VALUE. (LIST 3)

FIG. 19

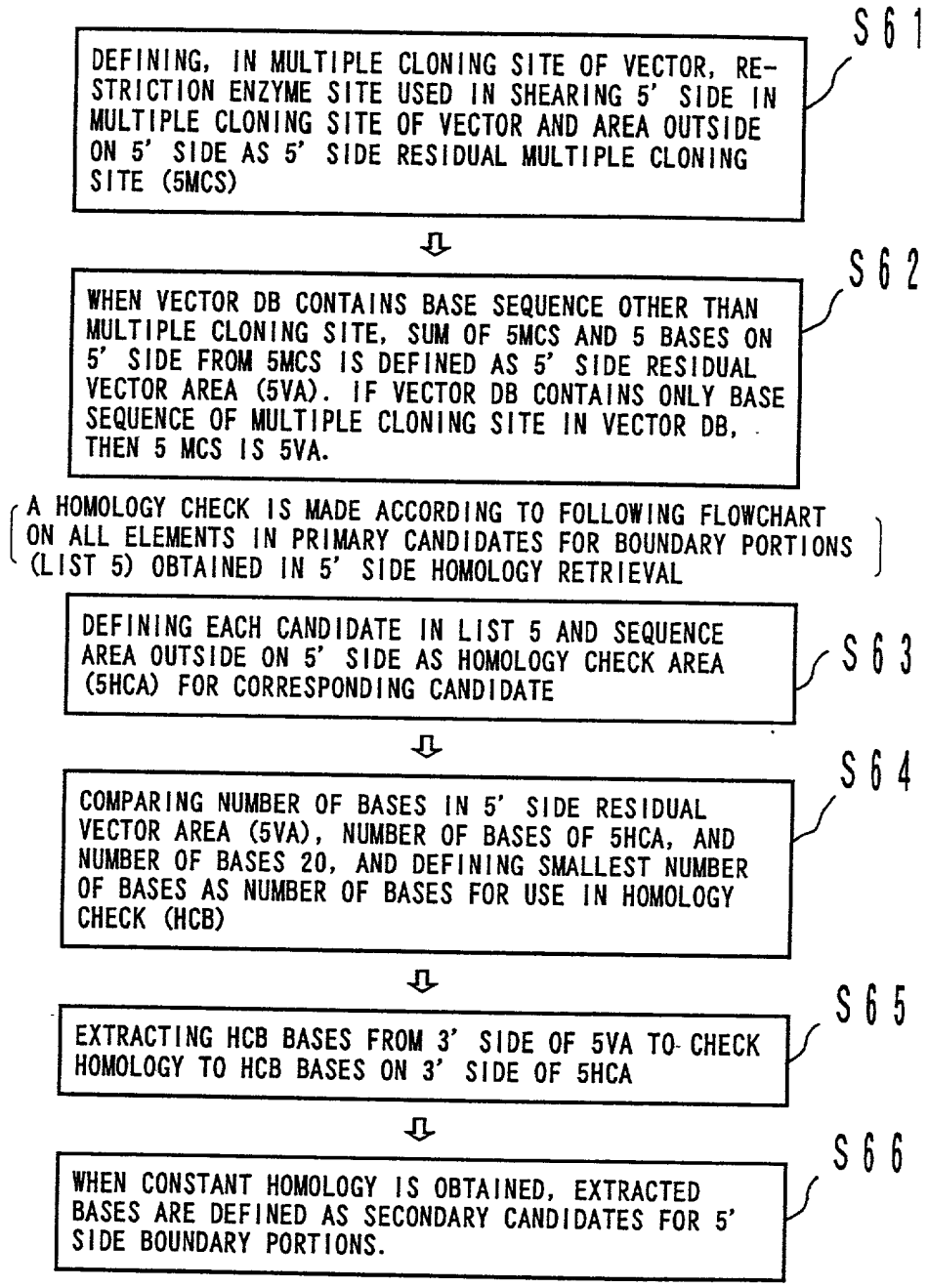
S61
DEFINING, IN MULTIPLE CLONING SITE OF VECTOR, RESTRICTION ENZYME SITE USED IN SHEARING 5' SIDE IN MULTIPLE CLONING SITE OF VECTOR AND AREA OUTSIDE ON 5' SIDE AS 5' SIDE RESIDUAL MULTIPLE CLONING SITE (5MCS)
S62
WHEN VECTOR DB CONTAINS BASE SEQUENCE OTHER THAN MULTIPLE CLONING SITE, SUM OF 5MCS AND 5 BASES ON 5' SIDE FROM 5MCS IS DEFINED AS 5' SIDE RESIDUAL VECTOR AREA (5VA). IF VECTOR DB CONTAINS ONLY BASE SEQUENCE OF MULTIPLE CLONING SITE IN VECTOR DB, THEN 5 MCS IS 5VA.
A HOMOLOGY CHECK IS MADE ACCORDING TO FOLLOWING FLOWCHART ON ALL ELEMENTS IN PRIMARY CANDIDATES FOR BOUNDARY PORTIONS (LIST 5) OBTAINED IN 5' SIDE HOMOLOGY RETRIEVAL
DEFINING EACH CANDIDATE IN LIST 5 AND SEQUENCE AREA OUTSIDE ON 5' SIDE AS HOMOLOGY CHECK AREA (5HCA) FOR CORRESPONDING CANDIDATE
S63
S64
COMPARING NUMBER OF BASES IN 5' SIDE RESIDUAL VECTOR AREA (5VA), NUMBER OF BASES OF 5HCA, AND NUMBER OF BASES 20, AND DEFINING SMALLEST NUMBER OF BASES AS NUMBER OF BASES FOR USE IN HOMOLOGY CHECK (HCB)
S65
EXTRACTING HCB BASES FROM 3' SIDE OF 5VA TO CHECK HOMOLOGY TO HCB BASES ON 3' SIDE OF 5HCA
S66
WHEN CONSTANT HOMOLOGY IS OBTAINED, EXTRACTED BASES ARE DEFINED AS SECONDARY CANDIDATES FOR 5' SIDE BOUNDARY PORTIONS.

FIG. 20

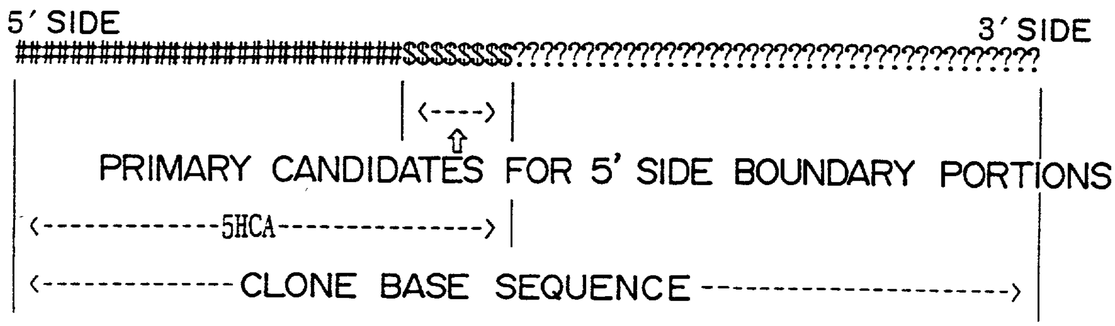
5′ SIDE
3′ SIDE
PRIMARY CANDIDATES FOR 5′ SIDE BOUNDARY PORTIONS
5HCA
CLONE BASE SEQUENCE

FIG. 21

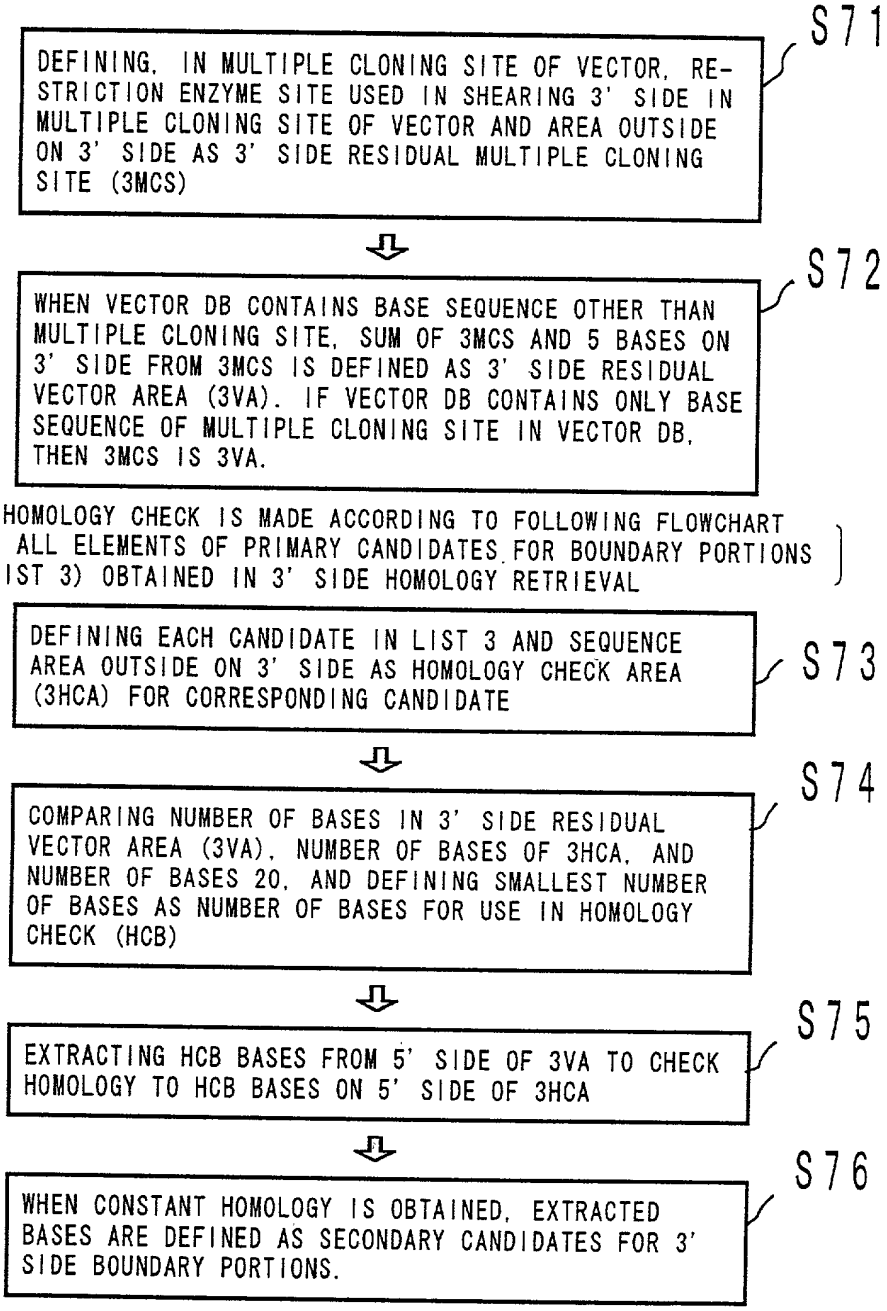
S71
DEFINING, IN MULTIPLE CLONING SITE OF VECTOR, RESTRICTION ENZYME SITE USED IN SHEARING 3' SIDE IN MULTIPLE CLONING SITE OF VECTOR AND AREA OUTSIDE ON 3' SIDE AS 3' SIDE RESIDUAL MULTIPLE CLONING SITE (3MCS)
S72
WHEN VECTOR DB CONTAINS BASE SEQUENCE OTHER THAN MULTIPLE CLONING SITE, SUM OF 3MCS AND 5 BASES ON 3' SIDE FROM 3MCS IS DEFINED AS 3' SIDE RESIDUAL VECTOR AREA (3VA). IF VECTOR DB CONTAINS ONLY BASE SEQUENCE OF MULTIPLE CLONING SITE IN VECTOR DB, THEN 3MCS IS 3VA.
A HOMOLOGY CHECK IS MADE ACCORDING TO FOLLOWING FLOWCHART ON ALL ELEMENTS OF PRIMARY CANDIDATES FOR BOUNDARY PORTIONS (LIST 3) OBTAINED IN 3' SIDE HOMOLOGY RETRIEVAL
S73
DEFINING EACH CANDIDATE IN LIST 3 AND SEQUENCE AREA OUTSIDE ON 3' SIDE AS HOMOLOGY CHECK AREA (3HCA) FOR CORRESPONDING CANDIDATE
S74
COMPARING NUMBER OF BASES IN 3' SIDE RESIDUAL VECTOR AREA (3VA), NUMBER OF BASES OF 3HCA, AND NUMBER OF BASES 20, AND DEFINING SMALLEST NUMBER OF BASES AS NUMBER OF BASES FOR USE IN HOMOLOGY CHECK (HCB)
S75
EXTRACTING HCB BASES FROM 5' SIDE OF 3VA TO CHECK HOMOLOGY TO HCB BASES ON 5' SIDE OF 3HCA
S76
WHEN CONSTANT HOMOLOGY IS OBTAINED, EXTRACTED BASES ARE DEFINED AS SECONDARY CANDIDATES FOR 3' SIDE BOUNDARY PORTIONS.

FIG. 22

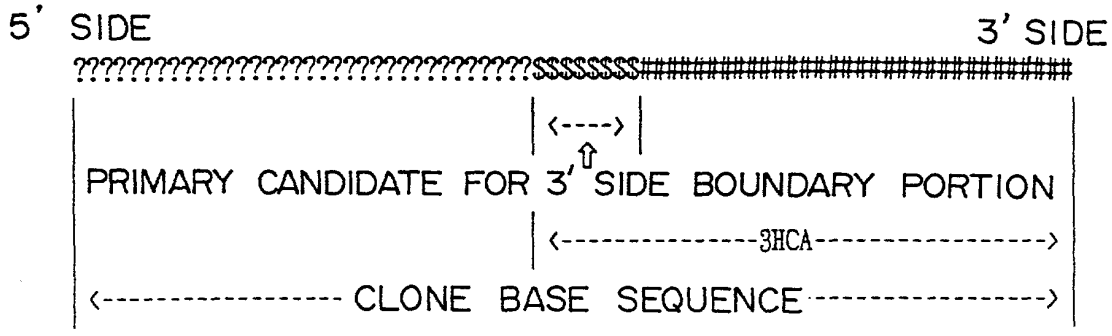
5' SIDE
3' SIDE
PRIMARY CANDIDATE FOR 3' SIDE BOUNDARY PORTION
3HCA
CLONE BASE SEQUENCE

FIG. 23

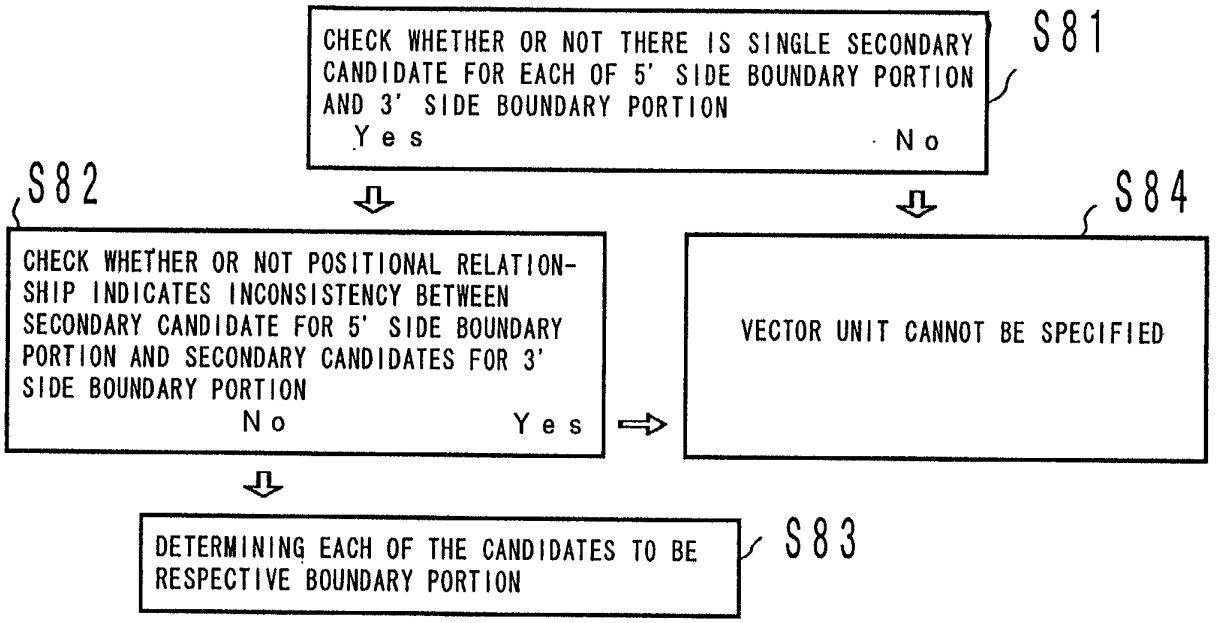
CHECK WHETHER OR NOT THERE IS SINGLE SECONDARY CANDIDATE FOR EACH OF 5' SIDE BOUNDARY PORTION AND 3' SIDE BOUNDARY PORTION
Yes
No
S81
S82
S84
CHECK WHETHER OR NOT POSITIONAL RELATION-SHIP INDICATES INCONSISTENCY BETWEEN SECONDARY CANDIDATE FOR 5' SIDE BOUNDARY PORTION AND SECONDARY CANDIDATES FOR 3' SIDE BOUNDARY PORTION
No
Yes
VECTOR UNIT CANNOT BE SPECIFIED
DETERMINING EACH OF THE CANDIDATES TO BE RESPECTIVE BOUNDARY PORTION
S83

FIG. 24

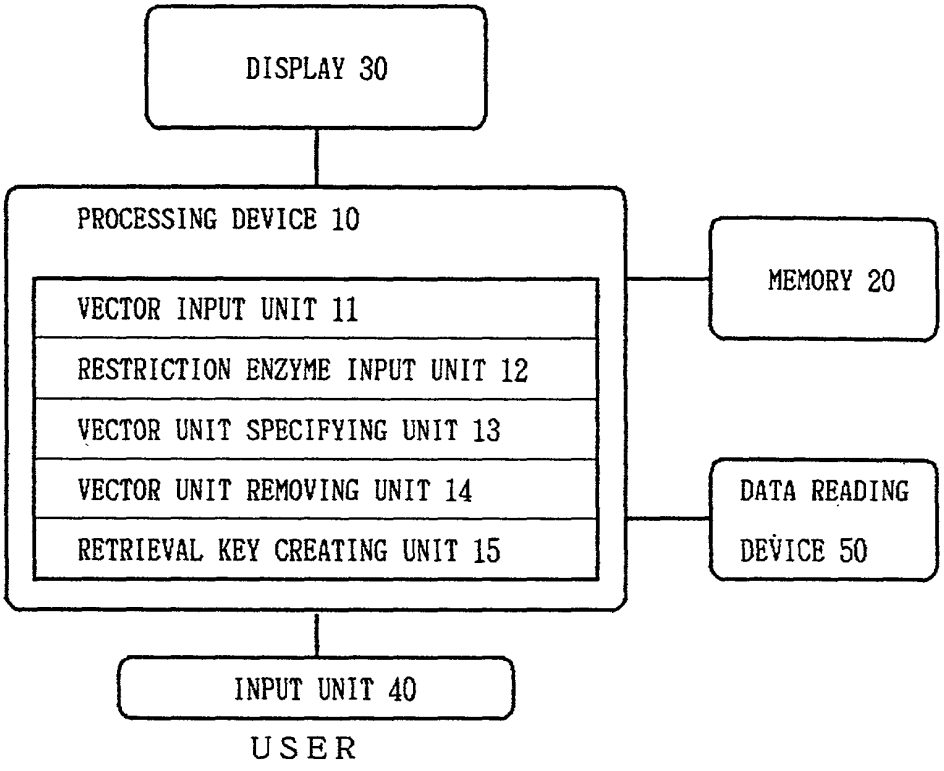
DISPLAY 30
PROCESSING DEVICE 10
VECTOR INPUT UNIT 11
RESTRICTION ENZYME INPUT UNIT 12
VECTOR UNIT SPECIFYING UNIT 13
VECTOR UNIT REMOVING UNIT 14
RETRIEVAL KEY CREATING UNIT 15
MEMORY 20
DATA READING DEVICE 50
INPUT UNIT 40
USER

FIG. 25